

Fig. 1

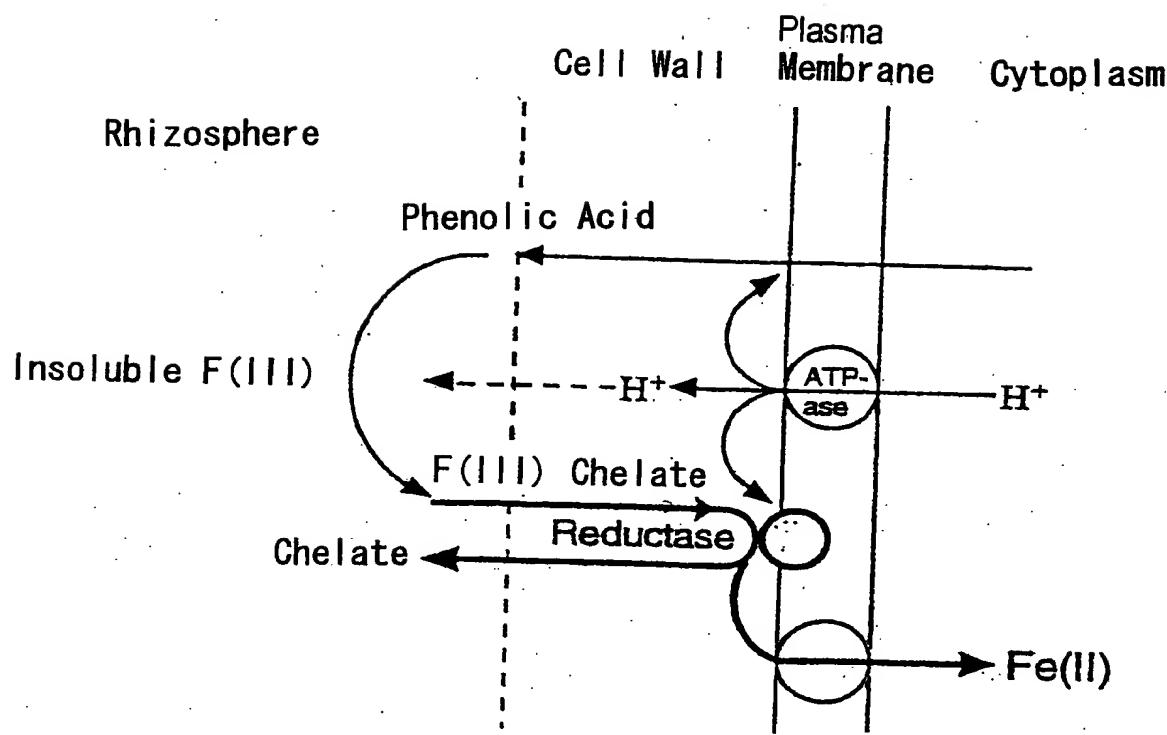
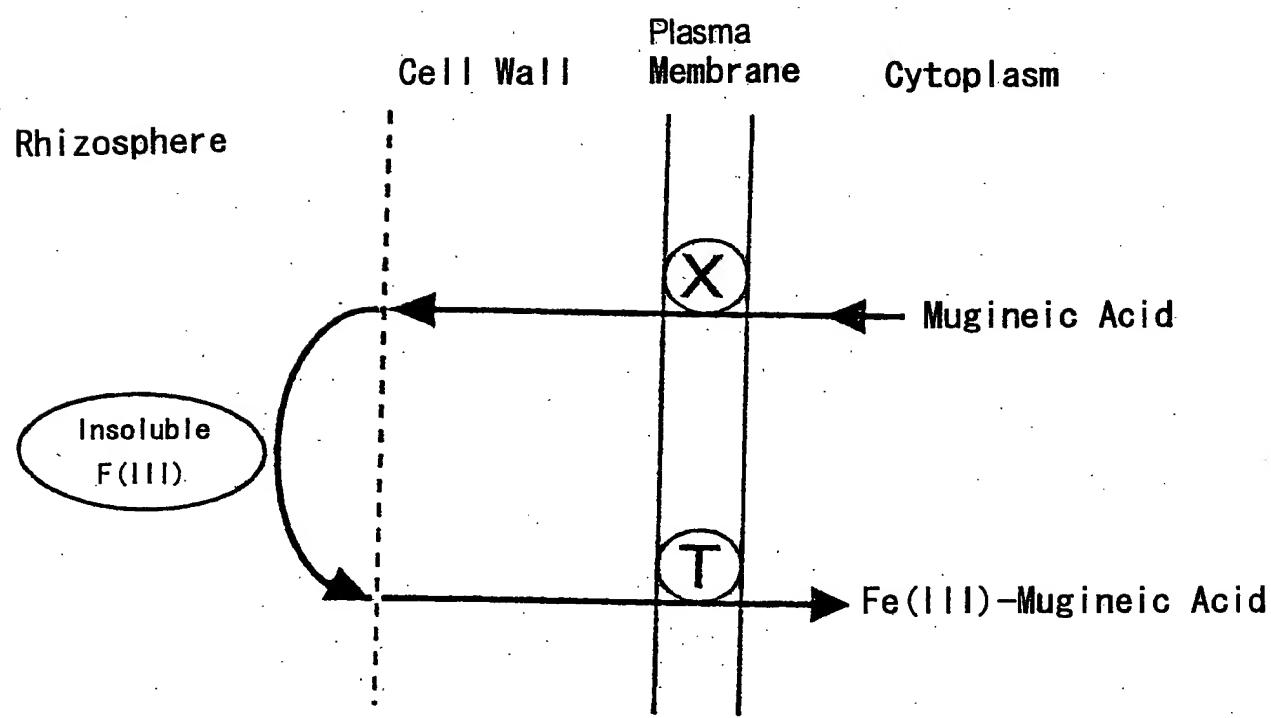


Fig. 2



Two Kinds of Fe-Uptake Mechanisms in Higher Plants

Fig. 3

putative poly(A) putative poly(A) putative poly(A)  
 poly(A) signal site poly(A) signal site poly(A) site  
 541 TCCGTC~~AAAAAA~~CACTTATT~~TT~~TCTGTTACAAAGATTAA~~TT~~ATGAAACGAACTTTTATT~~TT~~TGGAAGGCTTACCATTTA~~TT~~TT 630  
 181 S V K K S L I Y P S V Y K D Y N E R T F Y L W K R L P F N F 210

putative poly(A) poly(A) poly(A)  
 poly(A) signal site site site  
 631 ACAA~~CTCGAGGAAAGGCTCTCGT~~ATTAA~~TTTGT~~ATTATCTCTCAGTTGGTCAATAATTAAACTTCCACAC 720  
 211 T T R G K G L V V L I F V I L T I L S L S F G H N I K L P H 240

Fig. 4

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Fig. 5

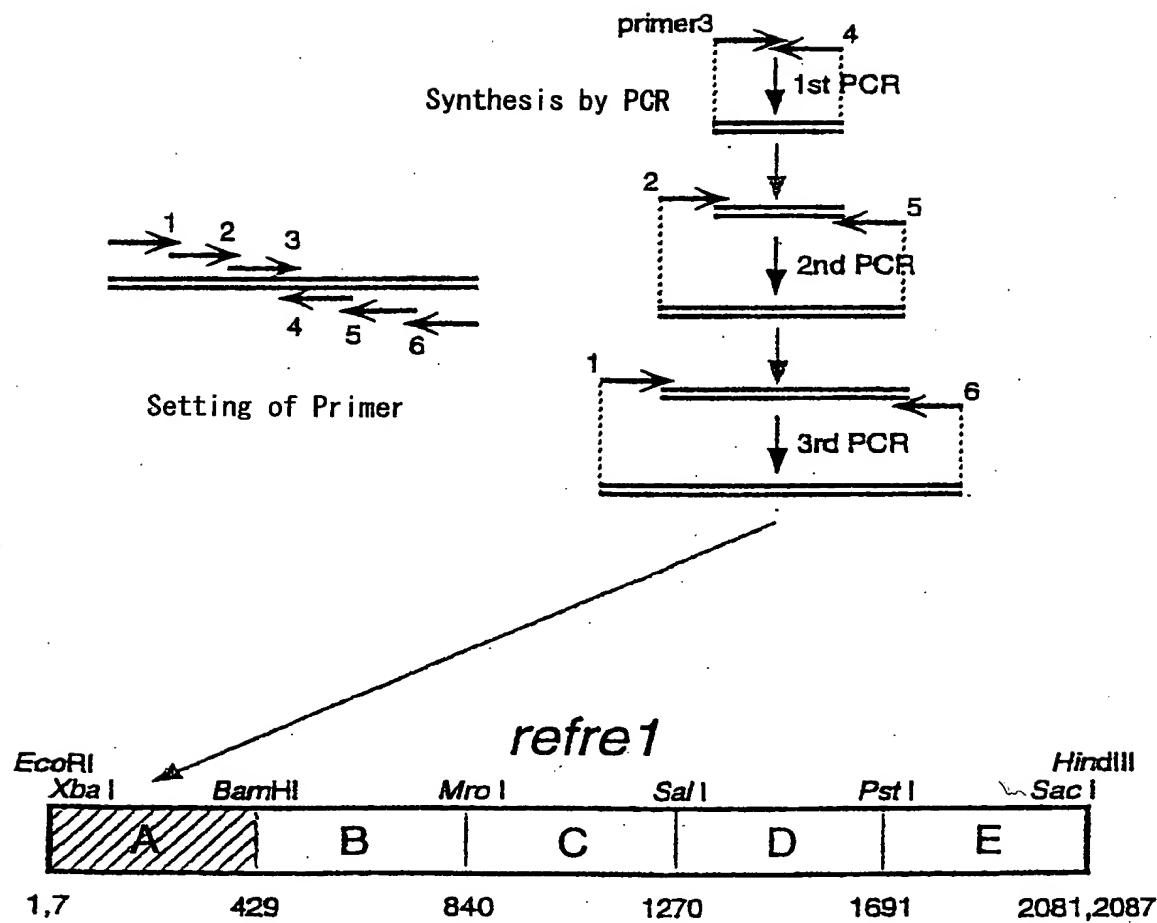


Fig. 6

## Sequence Name Base Sequence

		5'	3'	
A-1	GAATTCCTAGACTCCACCATGGTTAGAACCAAGAGTCCTTTCTGCTCTTCATCTCTTCTCTGCTACAGTCATGCGG			83mer
A-2	GTCATGAGGCGCTACACTCATCTGCACTTCATGCACTTCTCAGGCTGCACTGTCAGCTGCTGAGTCATGAGG			83mer
A-3	CAAGCAAGTCAAAGTCCTCTACTGCAAGAACATCAATTGGCTGGAAAGGCTACTGCACTGGCTTATGAGAACCTCAATCT			83mer
A-4	TCCAGTGTGAAACCTTGATACCTTGCTGGCTGGCAAGGTTCTCAAAAGCGGAGTCAGAGTCCTGTTAGATTGGAGTT			83mer
A-5	TGTCTCTATCGATTTCAGGAGCGGAAGGTAGTTACTTCATTAAGGTAGATGTTCTTCATGTCCTCCAGTGTGTTAA			83mer
A-6	GGATCCATAGTTCTCATAGTAGTAGTAGTGATAGGCGCTCTCATTTGOCATCAACGGTTGTGAAACAACTGTCCTTATCG			83mer
B-1	GGATCCACTTGAATTGATGOGATCTCAATGGTGCGCATGGGCGCTCGTCCTCTCTGGGTGCGAGTCCTAACGGCGCA			80mer
B-2	CTTAACTGGCGCAACTATCTTGACATCTCAAAACGGTATGGCAAGAACATTATGGCAATTCTGTTAAGAACGTC			80mer
B-3	GTTAAGAAGTCCTCTATCTACCCAAGGTTTACAAAGACTACAGGAGAGAACCTTCTATCTTGGAAACGTTGGCATT			80mer
B-4	AGAGTGAGAGAAATAGTCAGAATGACAAAGATAAGAAACTACGAGTCCTTGGCTTGAGTTGTAAGTTGATGGCAAACGT			80mer
B-5	AATGCCATGTATCTCTCATCTAGGTCTATGTAAGGATGGCAACTTGTATGTTATGTCGAAAGAGAGTGAGAGAAAT			80mer
B-6	TCCGGATAACCGAAAGGTACACCAAGGGAAAAGAGOGATTGGCATCAAGTCAGCACGGGTGAGAGAATGOCATTGAT			80mer
C-1	TCGGAAACAAACCTCTCATCCATCAACGGATTGAGCTTGTACTCTCACTTTACCAAAAGTCAGCATAGTC			83mer
C-2	GCATAOGCTCTCTCATGTTAGCGGTGCTCCATCAATGGTTTACGGCGCTTCAGGGTTAAACGGGAGTATTCAGTC			83mer
C-3	TATCCAGTCCTCTGTAAGGAAATTCTACTCTCAGATGGGAATAGTAGOCACAAATTCTTATGTCATCATCATTTCCAGTC			83mer
C-4	ATAAACATGTGTTCTACGGCTTGTGATAAGTAAGAAGATTCTAAACCTCGTTCTGAGAAGCTCTGGACTGGAAAAT			83mer
C-5	GAGGATGOCAGOCATGGGAGCAGATCCAGGCCATCCATCTAGTGTGTTGGCAATGTAATACATAGCTATGATAAACATGATGT			83mer
C-6	GTCGACAAAGTGGGGCTTAAAGACCTCGTTCTGATGATACTACAATTGGCAGAACCTGTCGAAGCAGAGGATGCG			83mer
D-1	GTGACCCACAGATGATTCTAACGTTATCAAGATCTCTGTCAGAACGGCTAACGTTCTCAAGTATCAAGTGGAGCATTTGCC			82mer
D-2	GGAGCATTTGCTATATGACTTTCTTCAACAAAATCAGCTGGTTCTACAGTTCTAACATCTCATCCCTCACAGTCCTAT			82mer
D-3	TTCACAGTCCTATCAGAAGGCACAGAGATCTAACACCCAGCACTAAACTATGTCAGTCAGCTAACAGGCCATTA			82mer
D-4	CCCTCTAAGAAAATCTGCAATCAACGGTATGGTTGGAGGCTTAGAACCTTCTGTAAGAAGTACTCTGTAATGCCCCTGTT			82mer
D-5	GGCGCGCACTACTCTACTAGATTCTCTTAAGTTGGCAATGAGGAGCACGTTAGGCCATATGGTCCTCTAAGAAAAT			82mer
D-6	CTCGAGTGTGATCAGTCTAGGCAATCTAACGCCATTCTACGAAATGGGGTAGATGGCTGCGACGCGGGCGAGCTACT			82mer
E-1	CTGCAACACAGTTCTACTGATGTCAGAACGGCTTAGTCACCTTAAGTGGTGGAAACGGAGCTACAATGGCTAA			77mer
E-2	ACAATGGCTTAAGGAGAAATCTTGTGAGTCCTCTGTCATCTACAGTGGGCTACAGTGGAGGATACAAACCTCAGATG			77mer
E-3	CAAACCTCAGATGAGTCACTAAGGTTTGGATGACAAAGGAAGATCTGAAATCAGCTGAAATGCGTAGAATGCTTAACAGAGG			77mer
E-4	GTGATGTTGTTCTGAGTTCTGACAAATTGATCTCTGATCTACAGTCAGTCCTTGAGGTCCTGGCTCTGTTAAG			77mer
E-5	CGATACCTTGACACTGCAATTCTAACAGTCATGGAAAGTGGCTGGCGATGAGTAGAAAGTGTGTTGTTG			77mer
E-6	AAGCTTGAGCTTACCAAGTAAAACCTCTCTCTAGTTGACATCTATCTCAGACTAGAAATGATAACCTTGTA			77mer

Fig. 7

Fig. 8

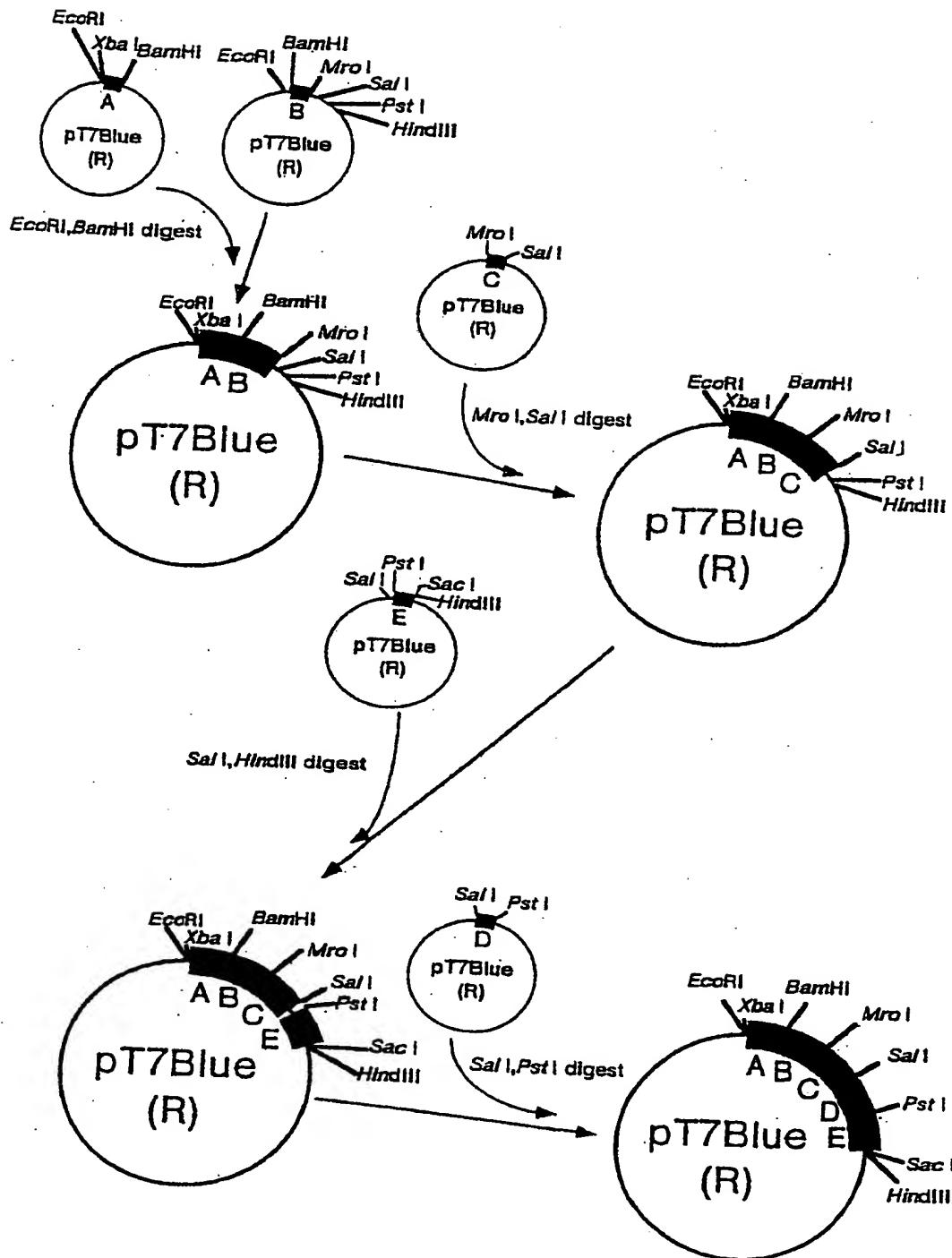


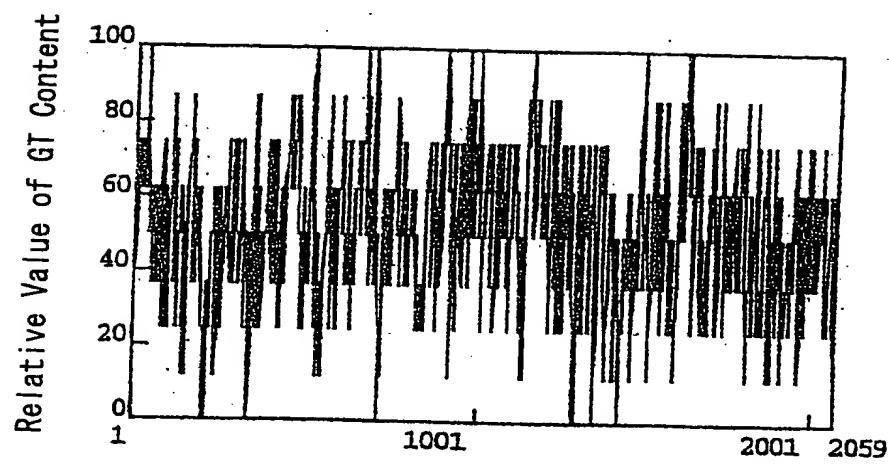
Fig. 9

1	gaattctcttagactccaa	19
20	ATGGTTAGAACCGAGCTCTTCTGCTCTTCATCTCTTCTGGTACAGTCCAAATCGAGCGGTACACTCATCTCCACTTCATT	109
	I M V R T R V L F C L F I S F F A T V Q S S A T L I S T S C I	30
110	TCTCAGGCTCTCACTGTACCGATTGGTCAAGCAAGTCMAAGCTCTTGCTACTGCAAGAACATCAATTGGCTCGGAAGGGTCACTGCA	199
31	S Q A A L Y O F G C S S K S K S C Y C K N I N W L G S V T A	60
200	TGCGCTTATGAGAACATCCAAATCTAACAGACTCTGGATCTCCGCTTATGAAACTTGCAAGCCAATGCTCAAGTATCAAGGTTTACACA	289
61	G I C A Y E N S K S N K T L D S A L N K L A S Q C S S I K V Y T	90
290	CTGGAGGACATGAGAACATCTACCTTAAATGCAAGTAACTACCTTGGCGCTCTGGAGAAATCCGATAAAGAAGACAGTTGTTTACAACCG	379
91	L E D B K N I Y L N A S H Y L R A P E K S D K K T V V S O P	120
380	TTCATGCCAAATGAGAACGCCATCTACTACTATGAGGAAACATATGGATCCACTTGATTTGATGCCATTCATGGTGCGATGG	469
121	L M A N E T A Y H Y Y Y E E H Y G I H L N L M R S O W C A W	150
470	GGCTCGCTCTCTGGTCCGAGTCCTTACCGCCGCACTATCTCTGAACTCTCAACGGTATTGGCAAGAACATTATGCCAAAT	559
151	G L V F F B V A Y L T A A T I L N I L K R Y F G K N I H A N	180
560	TCTGTTAAAGAAGCTCTTATCTACCAAGCGTTTACAAAGACTACACAGAGAGACTCTCTATCTTGGAAAGCTTGGCATTCACCTT	649
181	S V K K S L I Y P S V Y K D O Y H E R T F Y L W K R L P F N F	210
650	ACAACCTGGGCAAGGACTCGTAGTTCTTATCTTGTGCACTCTGACTATCTCTCACTCTCTTGGGACATAACATCAAGTTGGCACAT	739
211	T T R G K S L V V L I F V I L T I L S L S F G H N I K L P H	240
740	CCCTTACGATAGACCTAGATGGAGAAGATCAATGGCATTCGTCCTCACGGCGTGCTGACTTGATGGCAATCGCTTCTCCGGACATAACATCAAGTTGGCACAT	829
241	P Y D R P R W R R S M A F V S R R A D L B A I A L F P V V Y	270
830	CTTTGGTATCGGAAACACCCCTTCATCCAAATCACCGGATTGAGCTTGTACTCTCAACTTTTACACAAATGGTCAGCATACGTC	919
271	L F G I R N N P F I P I T G L S F S T F N F Y H K W S A Y V	300
920	TGCTTCACTGTTAGCGCTGTCATTCATCGTTATGACCGCTTCAGGTTAAACGAGGATATTCCAGTCTCTGTAAGGAAATCTAC	1009
301	C F M L A V V H S I V B T A S G V K R G V F Q S L V R K F Y	330
1010	TTCAGATGGGAATASTAGCCACAATTCTATGTCATCATTCATTCAGTCAGGCTTCAGGAACTTAAAGGATGGATGGCTGGATCTGG	1099
331	F R B G I V A Y T I L H S I I I F O S E K V F R N R B Y E I F	360
1100	TTACTTATTCAACAAAGCCATGAAACATCATGTTATCATAGCTATGTATTACCATGGCACACACTAAGGATGGATGGCTGGATCTGG	1189
361	L L I H K A M N I M F I I A M Y Y H C T L G W H G W I S	390
1190	ATGGCTGGCACTCTCTGACAGGTTCTGGAAATTGAGGTATCATGAAACGGAGGCTTAAGACCGCCACTTTGGGACCA	1279
391	M A G I L C F D R F C R I V R I F H N G G L K T A T L S T T	420
1280	GATGATTCTAACGTTATCAAGATCTCTGTCAGAACGCTAAGTCTCTCAAGTATGAGGGACATTGGCTATATGTACTCTCTICA	1369
421	D D S R V I K I S V K K P K F F K Y O V G A F A Y H Y F L S	450
1370	CCAAAATCAGCTGGTCTACAGTTCTACATCTACCCCTCACAGTCATCATGAAAGGCACAGAGATCTAACACCCAGATCACTA	1459
451	P K S A W F Y S F Q S H P F T V L S E R H R D P N H P D Q L	480
1460	ACTATGTAGCTAACGTAACAAGGCATTACGAGAGACTCTTGGCAAGTCTTAACGCTCCAAACCATACGGTTGATGGAGATT	1549
481	T H Y Y K A N K G I T R V L L S K V L S A P N H T V D C K I	510
1550	TCTCTAGAGGGACCATATGGCTAATGCTTCCATCACATTGCAAACTTAAGGAAATCTAGTGGAGTGGCTGGCGTGGCGTGGCA	1639
511	F L E G P Y G V T V P H I A K L K A N L V G V A A G L G V A	540
1640	GCATCTACCCCCATTCGAGAATGCCCTAGATTGCCCTAGCACTGATCACTGCAGGACAAGTCTACTGGATGGCTAACGACCTAGT	1729
541	A I Y P H F V E C L R L P S T O Q L Q H K F Y H I V N D L S	570
1730	CACCTTAAGTGTGTTGAAACAGAGCTAACATGGCTTAAGGAGAAATCTGTGAAGTCTCTGTCATCTACACTGGGTCATCAGTGGAGAT	1819
571	H L K I F E N E L Q W L K E K S C E V S V I Y T G S S V E D	600
1820	ACAAACTCAGATGAGTCCACTAAGGGTTCTGATGACAAGGAATCTGAAATCACCGTAGAAATGCCCTAACAGAGGCCAGACCTCAA	1909
601	T N S D E S T K G F D D K E E S E I T V E C L N K R P D L K	630
1910	GAGCTAGTGAAGATCAGAGATCAAATTGTCAAGAACCTGAGAACACACATCACTCTTACTCATCGGACCGGGACTTCAATGAGGAC	1999
631	E L V R S E I K L S E L E N N N I T F Y S C G P A T F H D D	660
2000	TTAGGAATCAGTTGATCAAGGATCGATTCTGAGATAGATGTCAGAAGCTAGAGGGAGGAGTTTACTTGGTAAGAGATCAAG	2089
661	F R M A V V Q G I D S S L K I D V E L E E E S F T B	687
2090	ctt	2092

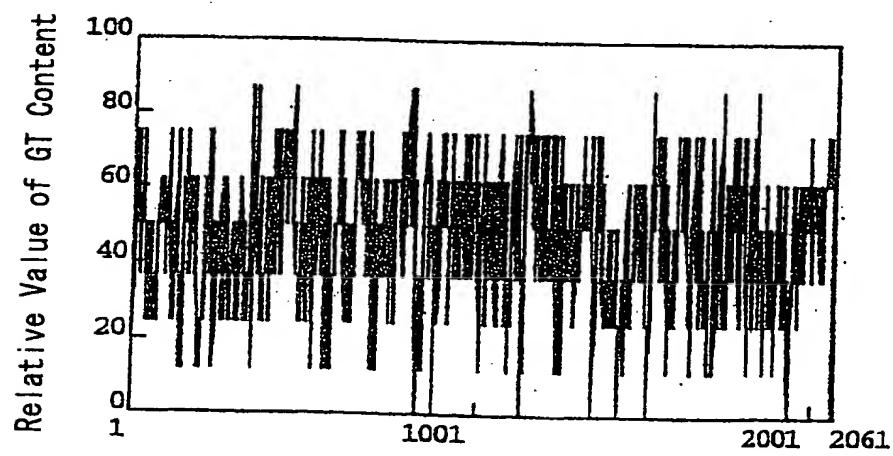
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Fig. 10

*FRE1*

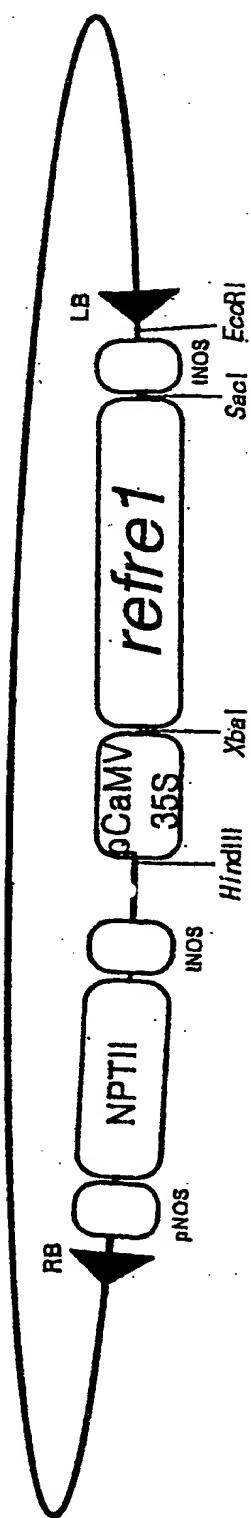


*refre1*



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Fig. 11



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Fig. 12



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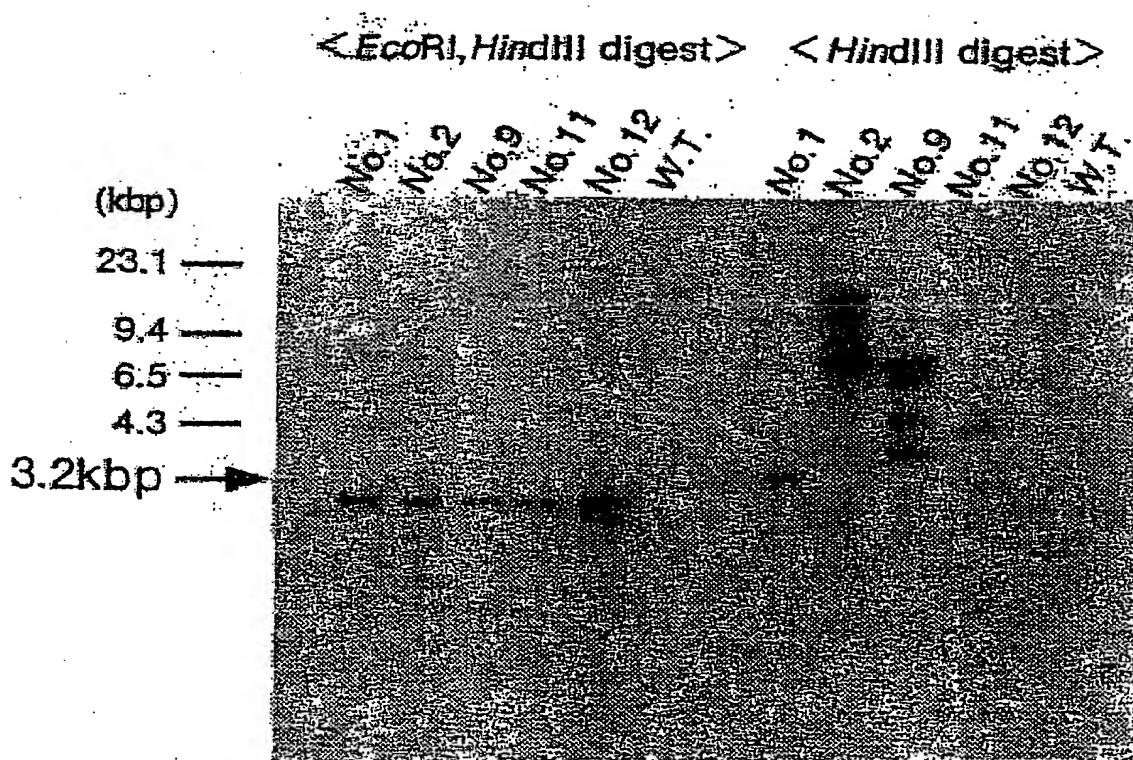
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Fig. 13



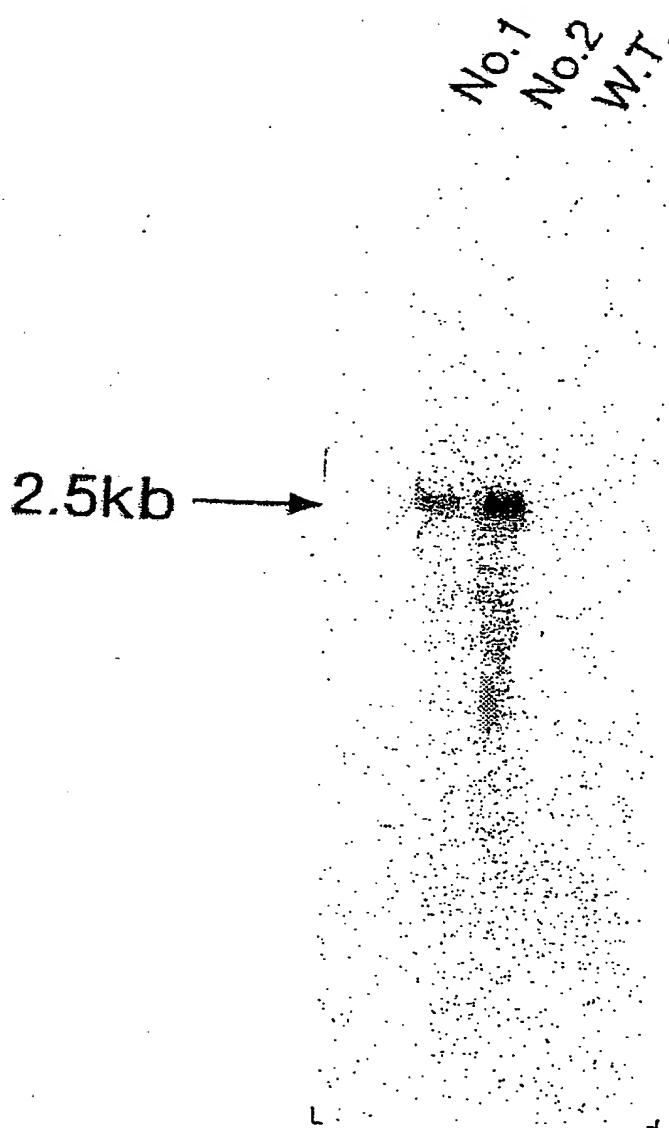
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Fig. 14



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Fig. 15



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Fig. 16



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Fig. 17



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Fig. 18



T<sub>2</sub> Plants